

## WE CLAIM:

1. A composition comprising a protein in crystalline form having unit cell dimensions, +/- 5%, of  $a=88.80\text{\AA}$   $b=88.80\text{\AA}$  and  $c=174.99\text{\AA}$ ,  $\alpha=\beta=\gamma=90$  wherein at least a portion of the protein has at least 90% identity with residues 16-314 of SEQ. ID No. 1.
2. A composition according to claim 1 wherein at least a portion of the protein has at least 95% identity with residues 16-314 of SEQ. ID No. 1.
3. A composition according to claim 1 wherein the protein comprises consecutively of residues 16-314 of SEQ. ID No. 1.
4. A composition according to claim 1 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.
5. A composition according to claim 1 wherein the protein crystal has a crystal lattice in a  $P4_122$  space group.
6. A method for forming a crystal of a protein comprising:  
forming a crystallization volume comprising: a precipitant solution and a protein wherein at least a portion of the protein has at least 90% identity with residues 16-314 of SEQ. ID No. 1;  
storing the crystallization volume under conditions suitable for crystal formation of the protein; and  
forming a crystalline form of the protein having unit cell dimensions, +/- 5%, of  $a=88.80\text{\AA}$   $b=88.80\text{\AA}$  and  $c=174.99\text{\AA}$ ,  $\alpha=\beta=\gamma=90$ .
7. A method according to claim 6 wherein at least a portion of the protein has at least 95% identity with residues 16-314 of SEQ. ID No. 1.

8. A method according to claim 6 wherein at least a portion of the protein comprises consecutively of residues 16-314 of SEQ. ID No. 1.
9. A method according to claim 6 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.
10. A method according to claim 6 wherein the protein crystal has a crystal lattice in a  $P4_122$  space group.
11. A method comprising:  
diffracting a protein in crystalline form having unit cell dimensions, +/- 5%, of  $a=88.80\text{\AA}$   $b=88.80\text{\AA}$  and  $c=174.99\text{\AA}$ ,  $\alpha=\beta=\gamma=90$  wherein at least a portion of the protein has at least 90% identity with residues 16-314 of SEQ. ID No. 1; and  
solving the structure of the protein from the diffraction pattern.
12. A method according to claim 11 wherein at least a portion of the protein has at least 95% identity with residues 16-314 of SEQ. ID No. 1.
13. A method according to claim 11 wherein at least a portion of the protein comprises consecutively of residues 16-314 of SEQ. ID No. 1.
14. A method according to claim 11 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.
15. A method according to claim 11 wherein the protein crystal has a crystal lattice in a  $P4_122$  space group.